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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          1605
1129
917.5
913.5
257
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224
224
224
                                                                                                                                                                                                                                                        Score
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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.
        92.6
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52.9
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SIDSB/gcgdata/geneseq/geneseqp/AA198.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA198.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA198.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA199.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA199.DAT:*
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Listing first 45 summaries
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1733
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Copyright (c) 1993 - 2000 Compugen Ltd
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\(\SIDS8\)/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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      AAW05409
AAR85919
AAW72071
AAR77439
AAW54313
AAB12071
AAW18063
AAW18063
AAW14004
AAW142070
AAR84636
                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Human Crk-like pro
Mouse CRKL protein
NH2-terminal c-CRK
SH3 domain from v-
Growth factor rece
Human GRB-2. Homo
Growth factor rece
Grb2 protein. Hom
                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                           Human GRB-3.
                                                                                                                                                                                                            Mouse Crk protein.
                                                                                                                                                                                           Homo
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CD2-associated	AAW25115 AAW80419	18 20	553 553	8. 1.1	141 141
	AAW26495	18	553	. 1	141
Rat phosphodieste	116	21	1683	8.2	141.5
Human	992	15	870	8.3	143.5
	AAR25336	13	1047	œ (144.5
GAP6 encoded	AAR11137	12	1047	ω (144.5
Segmente of	~ (1 ;	1047	ω c	144.5
Bootide Esezi	AA1U/4UU	7 1	217	ນ ເ	1447
Mouse Ese2) K	1650 177	ο α η υ	147
Mouse	AAW05393	17	788	8.5	147.5
Human	AAB66391	22	464	8.6	149
CD2 associated	AAW80420	20	464	8.6	149
	AAW25116	18	464	8.6	149
CD2 as	AAW26496	18	464	8.6	149
Human	AAW76830	19	330	8.7	151.5
Mouse	AAY57444	21	1214	8.8	152
Mouse Esell	AAY57449	21	1715	8.9	154.5
Amino	AAY69388	21	330	9.0	156.5
Human	AAY32154	20	1144	9.1	157
Human	AAY32158	20	641	9.1	157
Human	AAW05399	17	509	9.1	157
Human	AAW05395	17	462	9.1	157
Human	AAY32155	20	1220	9.1	158
Human	AAY32156	20	1215	9.1	158
Human	~1	21	330	9.1	158.5
Human	AAY22237	20	847	9.2	159.5
Human		20	287	9.2	159.5
Mouse vav j	AAR25671	ű	844	9.6	167
Amino	AAY27125	20	797	10.0	172.5
PKA substra	AAY49419	21	845	10.0	174
Phosphol	AAR90583	17	1290	10.2	177
Growth	AAR26061	13	317	12.1	210

ALIGNMENTS

AAW05409 RESULT

standard; Protein;

304

ΑA

Mouse Crk protein.

23-FEB-1998 (first entry)

AAW05409; AAW05409

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Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process.
                             03-APR-1996;
07-APR-1995;
                                                                                                                          Misc-difference
(CYTO-) CYTOGEN CORP. (UYNC-) UNIV NORTH CAROLINA.
                                                         04-APR-1996;
                                                                            10-OCT-1996
                                                                                              W09631625-A1
                                                                                                                                             Misc-difference
                                                                                                                                                                        Mus musculus.
                            96US-0630915.
95US-0417872.
                                                        96WO-US04454.
                                                                                                                         /note= "encoded by GAC" 168
                                                                                                                                            Location/Qualifiers
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RESULT
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AC AAR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC domain containing proteins that can be used in the method of the cinvention. SH3 domain containing proteins play a role in signalling and convention. SH3 domain containing proteins play a role in signalling and containing proteins play a role in signalling and containing functional domains of interest contactural elements of cells. The method of the invention is for cleantifying polypeptides containing functional domains of interest contacting a multivalent contacting a multivalent contacting a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence contacting a multivalent contain an SH3 domain due to the minimal sequence contains which contain an SH3 domain due to the minimal sequence contains which contain an SH3 domain due to the minimal sequence contains which contain an SH3 proteins. It has been found that small peptide contain compared to monomer RUs. Multivalent RU complexes are particularly contain compared to monomer RUs. Multivalent RU complexes are particularly contained to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target contained to be identified. Identification of novel SH3 proteins will be consecuted and contain the processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 302
                  AAR85919;
                                                AAR85919 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying polypeptide(s) having specific f SH3 domain) - comprises detecting selective unit, regardless of sequence homology
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                                                                                                                                                                                                                                                                                                                                                                                  INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS 124
                                                                                                                                                              DFS 307
                                                                                                                                                                                                                                                                       IPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYAR
                                                                                                                                                                                                                                                                                                                                     RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM
                                                                                                                                                                                            viqkrvpnaydktalalevgelvkvtkinvsgqwegecngkrghfpfthvrlldgqnpde
                                                                                                                                                                                                                                                       ipvpyvekyrpasasvsaliggnqegshpqplggpepgpyaqpsvntplpnlqngpiyar
                                                                                                                                                                                                                                                                                                                      rggsgvilrqeeaeyvralfdfngndeedlpfkkgdilrirdkpeegwwnaedsegkrgm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1605; DB 17;
Pred. No. 2.1e-134;
0; Mismatches 1;
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RESULT
AAW42071
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   04-JUN-1998
                                                           AAW42071;
                                                                                                                    AAW42071 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 34A-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding tyrosine kinase-binding proteins – used to screen agents capable of modulating cell growth or cellular metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS
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                                                                                                                    Protein;
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98.2%;
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Pred. No. 2.7e-92;
0; Mismatches 4;
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Best Local S
Matches 185
                                                                                                                                                                                                                                                                                                                This is the sequence of human Crkl. Translation of Crkl cDNA can linhibited by oligonucleotides of specific composition that hybridise to its translation initiation site. The oligonucleotide compositions can be used for treating, particularly chronic myelogenous leukaemia (CML). See AAV09216.
                                                                                                                                                                                                                                                                                                                                                                                                                        Use of anti-sense oligo:nucleotide(s) to Grb2 or Crk1 nucleic acids for inhibiting growth of cancer cells in treatment of cancers,
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                particularly chronic myelogenous leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crk-like; Crkl; CML; translation initiation site; bcr-abl;
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arlinghaus RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Crk-like protein Crkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9801547-A1
                                                                                             106
                                              166
 216
                                                                                                                    124
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                                                                                         psppmgsvsapnlptaednleyvrtlydfpgndaedlpfkkgeilviiekpeegwwsarn
                                                                                                                                                                                                AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI
                                                         -----SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAED
lpavsgspgaaitplpstqngpvfakaiqkrvpcaydktalalevgdivkvtrmningqw
                                                                                                                                                                                      sarfdssdrsawymgpvsrqeaqtrlqgqrhgmflvrdsstcpgdyvlsvsensrvshyi
                                                                                                                                                               INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myelogenous leukaemia;
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV09214.
                                                                                                                                                                                                                                                                                               303 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Fig 5; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US10101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
78..101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lopez-Berestein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238..290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SH2'
131..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 14..64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SH3
/note= "This domain is designated SH4 in the disclosure"
             -TPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SH3
                                                                                                                                                                                                                                               52.9%; Score 917.5; DB 1 56.6%; Pred. No. 1.9e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         = SH2
                                                                                                                                      --rfkigdqefdhlpallefykihyldtttliepapry
                                             lvrssphgkhgnrnsnsygipepahayaqpqtttp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer.
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                            DB 19; Length 303;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                   Gaps
                                                                                                                 177
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  275
                                              215
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Query Match
Best Local
                                                                                      leukaemia. Thus, overexpression of tyrosine-phosphorylated CRKL protein, or an increase in protein, gene copy number or mRNA is indicative of ph-positive leukaemia. Fragments of the CRKL protein may also be used in the treatment of individuals with cancers arising from cells which express the CRKL protein by inhibition of
                                                                                                                                                   The mouse CRKL protein may be used in the diagnosis of Philadelphia chromosome-positive leukaemias. For example, since CRKL is clearly tyrosine-phosphorylated in chronic myelogenous leukaemia and philadelphia chromosome (Ph)-positive acute lymphoblastic leukaemia patients expressing the BCR/ABL protein, but not in BCR-ABL-negative peripheral blood cells, tyrosine-phosphorylation of CRKL may be used as a diagnostic indicator for BCL/ABL activity in Ph-positive
                                                                                                                                                                                                                                                                                     Diagnosis of tyrosine phosphorylated CRKL protein cancers detecting increased level of CRKL protein or CRKL binding also compsns. for treating chronic myelogenous leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse CRKL protein; tyrosine phosphorylation; diagr
chronic myelogenous leukaemia; acute lymphoblastic
Philadelphia chromosome; BCL; ABL; treatment.
                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                               Groffen JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1996 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR77439 standard;
                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9531545-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse CRKL
                                                                                                                                                                                                                                                                                                                                                                                                         (CHIL-) CHILDRENS HOSPITAL LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279
                                                                           synthesis or activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGECNGKRGHFPFTHVRLLDQQNPDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                   303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-terminal SH3 domain"
193..210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "SH2 domain""
131..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                             74pp; English.
52.7%;
56.0%;
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                                                                                                                                                                                                                                                                                                                                                                                NC,
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Score 913.5; DB 1
Pred. No. 4.4e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                           CRKL protein
            DB 17;
             Length
              303;
                                                                                                                                                                                                                                                                                                  protein,
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Matches 183;

Similarity

Conservative

35;

Mismatches

56;

Gaps

6;

0;

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RESULT
AAM54313
AD
                                                                                                                                                  The peptides AAW54313-W54314 were used in the demonstration of the effect of a non-specific interaction on the identification of ligands for targets of interest. The identification of ligands or catalysts from a library can be used for detecting ligands such as proteins and coligonucleotides. The ligands obtained can be used as drugs and coligonucleotides. The ligands obtained can be used as drugs and coligonucleotides. The ligands obtained can be used as drugs and coligonucleotides.
                              for drug design. The catalysts obtained can be used e.g. to produce pharmaceuticals, materials such as plastics and other polymers, and other products such as food products, detergents and other cleansers oral hygiene products (e.g. toothpastes, mouthwashes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhancing the concentration of ligand for target molecule - usin library of potential ligands with binding pair member and target molecule with second binding pair member
                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-207532/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NECA-) NETHERLANDS CANCER INST. (WHED ) WHITEHEAD INST BIOMEDICAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW54313 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schumacher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c-CRK SH3 domain derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interaction; ligand; identification; catalyst; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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CC The present sequence is the SH3 domain from v-crk protein. A SH3
CC domain is also found in ratt RIZ (ARB12078). RIZ is retinoblastoma
CC (RB)-interacting zinc finger protein. RIZ is a nuclear phosphoprotein
CC that acts as a cell differentiation factor. RIZ can modulate cell growth
CC by binding to Rb protein, which is involved in regulating cell
CC proliferation. In addition, RIZ can act to regulate transcription. RIZ
CC functions to maintain cells in the G1 phase of the cell cycle, by
CC interacting with Rb through the cr2 domain of RIZ. Rat RIZ protein
CC contains a number of GTPase motifs (see ARB12037 to ARB12056 and ARB12099
CC to ARB12104). RIZ protein is a PR domain protein and is present primarily
CC in the cell nucleus. RIZ gene mutations may be implicated in various
CC cancers such as melanoma, neuroblastoma, leukaemia and breast cancer, and
CC cancers such as melanoma, neuroblastoma, leukaemia and breast cancer.
CC RIZ protein is implicated in cell cycle arrest, inhibition of RIZ
CC activity may be used in neurodegenerative disorder therapy e.g. for
CC activity may be used in neurodegenerative disorder therapy e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                             New PR domain peptides comprising amino acid sequences from, for example retinoblastoma-interacting zinc finger, or egl-43 proteins, regulating gene transcription and controlling cell proliferation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; cell proliferation; cell differentiation; tissue repair; transcription regulator; breast cancer; gene therapy; melanoma; neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease; Alzheimer's disease; paralysis; motor neurone disorder;
activity may Parkinson's,
                                                                                                                                                                                                                                                                Disclosure; Fig 2; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-410879/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-1994;
06-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3 domain from v-crk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (LJOL-) LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6069231-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Huntingdon's or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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95US-0399411.
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96.7%;
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 Alzheimer's
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Pred.
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No.
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disease,
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RESULT
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     Sequence (AAT67275) originally derived from a human tonsil CDNA
C library. It shows 58% identity with the human Grb2 amino acid
Sequence. Methods are claimed for producing pure human Grb2-1
C protein in a recombinant host cell, for treating conditions related
C to insufficient Grb2-1 protein function, and for identifying
C compounds that modulate Grb2-1 activity, such as substances that
C modulate the ras pathway in T-lymphocytes by affecting the binding
C of Grb2-1 to the cell membrane. Modulation of Grb2-1 function can
C be used to affect immune system function by affecting T-cell
C proliferation pathways. Antagonists have immunosuppressive
C activities and can be used to treat and prevent autoimmune diseases
C and transplant rejection. Agonists can be used to treat immune
C deficiency states such as HIV infection or cancer.
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Best Local
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                                                                                                                                                                                                                                                                                                                  Growth factor receptor-binding protein 2 homologue and related DNA used to develop products for diagnosis and therapy of, e.g. autoimmune diseases, transplant rejection, HIV infection or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth factor receptor-binding protein 2 homologue; Grb2-1; signal transduction; antagonist; antisense; immunosuppressiv autoimmune disease; transplant rejection; agonist; HIV; infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth
                                                                                                                                                                                                                          specificity.
                                                                                                                                                                                                                                         This polypeptide comprises a human growth factor receptor-binding protein 2 homologue, Grb2-1 (AAW18063), that exhibits T-cell
                                                                                                                                                                                                                                                                                       Claim 4; Page 38-39;
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-319539/29
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunnington D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurone disorders, or cardiac disorders e.g. heart disease, where the ability to induce neural/ cardiac tissue proliferation would be useful The present sequence was used for sequence homology comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(JOSL-) JOSLIN DIABETES CENT INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1997
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                                                                                                                                                                                                                       homologue, Grb2-1 (AAW18063), that exhibits T-cell
ty. Its amino acid sequence was deduced from a cDM
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                                                                                                                                                                                                                                                                                   57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoelson SE
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Pred. No. 6.
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ejection; agonist; HIV; infect
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                   Using a new cloning technique, CORT (cloning of receptor targets) several new tyrosine kinase (TK) binding proteins were isolated. Growth factor receptor bound proteins GRB-1, GRB-2, GRB-3, GRB-4, GRB-7 and GRB-10 were isolated using this method. This sequence represents GRB-2. The proteins bind to a tyrosine-phosphorylated domain of a eukaryotic TK. GRB proteins can be used for screening agents which are capable of modulating cell growth that occurs via signal transduction through TKs. Such agents can be used to prevent or inhibit cell growth or to counteract tumour development. GRB proteins are also useful for identifying susceptibility to diseases asociated with alterations in cellular metabolism mediated by TK pathways e.g. cancer and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRB-2; growth factor receptor bound; tyrosine kinase; regulation; cell growth; cellular metabolism; screening; signal transduction; cancer; diabetes; CORT technique; cloning of receptor targets.
                                                                                                                                                                                                                                                  DNA encoding tyrosine kinase-binding proteins – used to screen agents capable of modulating cell growth or cellular metabolism
                                                                                                                                                                                                                                                                                                   WPI; 1995-328235/42.
N-PSDB; AAT07167.
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                                                                                                                                                                                                                    Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                Margolis BL,
                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1994;
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                                                                                                                                                                                                                  215pp; English.
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Pred. No. 4.7e-15;
0; Mismatches 54
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Query Match Best Local (

Similarity

12.9%;

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27-SEP-1995;
30-NOV-1995;
09-APR-1996;
                Human epidermal growth factor receptor binding protein GRB2 (AAW14003) is an src homology domain 3 (SH3) protein that is capable of binding to novel murine and human SHIP (SH2-containing inositol phosphatase) proteins (see also AAW14002-03). It can be used in markhods for identifying agonists and antagonists of SHIP.
                                                                                                                                                                                                                                                                                                                                     SH2-containing inositol phosphatase; SHIP; Inositol polyphosphate 5-phosphatase; src homology domain SH2 domain; signal transduction; leukaemia; cancer; Grb2; epidermal growth factor receptor binding protein.
 Sequence
                                                                                                                                             WPI;
                                                                               Disclosure; Page 47-48; 89pp;
                                                                                                               Inositol
                                                                                                                                  N-PSDB;
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                                                                                                    treating
                                                                                                                                                               Krystal G
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DB; AAT60302.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRGMIPVPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGSGVILRQ-----EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
                                                                                                                                                                                   KRYSTAL
                                                                                                   polyphosphate-5-phosphatase having SH2 domain - useful fo cancer and other conditions involving abnormal signalling
  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                      96US-0664962.
95US-0006063.
95US-0007788.
96US-0015217.
                                                                                                                                                                                                                                                         96WO-CA00655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 224; DB
Pred. No. 4e-1
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57;
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                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
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Query Match

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Score 224;

DB 18;

Length

217;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW42070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Lo
                                                                                             Use of anti-sense oligo:nucleotide(s) to Grb2 or Crkl nucleic acids - for inhibiting growth of cancer cells in treatment of cancers, particularly chronic myelogenous leukaemia
                                                                                                                                                                                                                                                                                                                                                                            Growth factor
translation in
                                                                                                                                                                                                                                                                                                                                                                                                        Growth
                         This is a polypeptide sequence of Grb-2. Translation of Grb-2 cDNA can be inhibited by oligonucleotides of specific composition that hybridise to its translation initiation site (see AAV09215). The oligonucleotide compositions can be used for treating, particu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW42070 standard;
                                                                         Disclosure; Fig 4; 47pp; English.
                                                                                                                                   N-PSDB;
                                                                                                                                                              Arlinghaus RB,
                                                                                                                                                                                                     08-JUL-1996;
                                                                                                                                                                                                                       08-JUL-1997;
                                                                                                                                                                                                                                         15-JAN-1998
                                                                                                                                                                                                                                                            W09801547-A1
                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                 (TEXA ) UNIV TEXAS
                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRGMIPVPYV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q---iflrdieqvpqqptyvqalfdfdpqedgelgfrrgdfihvmdnsdpnwwkga-chg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1rdg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGSGVILRQ-----EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
                                                                                                                                                                                                                                                                                                                                                                                                       factor
                 myelogenous
                                                                                                                                   AAV09213
                                                                                                                                                                                                                                                                                                                                                                           or receptor-bound initiation site;
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        receptor-bound
                                                                                                                                                                                                     96US-0679437
                                                                                                                                                                                                                        97WO-US10101
                                                                                                                                                                                                                                                                                                          /label=
60..158
                                                                                                                                                              Lopez-Berestein
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 5..54
                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                 abel= SH2
                                                                                                                                                                                  SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                   leukaemia
                                                                                                                                                                                                                                                                                         . 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----agkyflwvvkfnslnelvdyhr----
                                                                                                                                                                                                                                                                                                                     SH3
                                                                                                                                                                                                                                                                                SH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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                                                                                                                                                                                                                                                                                                                                                                            protein 2; Grb-2; CML; bcr-abl;
chronic myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                        protein
                  (CML).
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                           treating, particularly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -sts---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -vsrnq
                                                                                                                                                                                                                                                                                                                                                                               cancer
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DB 19;

Length 217;

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RESULT 1
AAR84636
ID AAR8
        Query Match
Best Local S
Matches 53
The human Grb2 protein (AAR84636) acts as an adaptor to link BCR-ABL tyrosine-kinase to mSos1 (AAR8463B). The resulting BCR-ABL-Grb2-mSos1 complex activates the Ras pathway leading to morphological transformation. Substances that affect this transformation are useful in the treatment of chronic, acute myelogenous or acute lymphocytic leukaemia, and are identified by reaction with Grb2 (or its SH2 or SH3 domains) and with a cpd. contg. the Brb2-binding site on BCR-ABL, Sos or Shc and examination of any resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOUN )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grb2 protein
                                                                                                                                                                                                                                     Example 1; Page 48; 106pp; English.
                                                                                                                                                                                                                                                                                      Detection of agents that modify BCR-ABL mediated transformation useful in treatment of leukaemia and other malignancies
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arlinghaus R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR84636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR84636 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
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                                                                                                                                                                                                                                                                                                                                                                     1995-302931/40.
DB; AAT05108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \verb"q---iflrdieq" vpqqpty vqalfdfdpqedgelgfrrgdfihvmdnsdpnwwkga-chg" and a statement of the statement of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUNT SINAI HOSPITAL CORPUNIV TEXAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine kinase; transformation; Ras; oncoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SH3_domain
60..157
/label= SH2_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163..
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27.9%;
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Pred. No. 4e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                         /note=
Misc-difference 199
                                                                                                                            /note=
Misc-difference 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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06-AUG-1992
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                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                   Tyrosine phophorylation; src homology domain; SH2;
                                                                                                                                                                                                                                                                                         Growth Factor Receptor Bound protein GRB-2 partial sequence
                                                                                                                                                                                                                                                                                                         02-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                         AAR26061;
                                                                                                                                                                                                                                                                                                                                       AAR26061 standard;
               WO9213001-A
                                    Misc-difference
                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                         q---ifirdieqvpqqptyvqalfdfdpqedgelgfrrgdfihvmdnsdpnwwkga-chg
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301
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302
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299
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196
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133
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                             /note=
                                            'note-
                                                                                                                      'note=
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                                                                                                                                                                                "corresponds to CNG codon, where N is unknown"
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                                                                                                                                                                                                                                                                   epidermal growth factor receptor; SH3.
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Pred. No. 6e-12;
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RESULT 1
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Best Local
                                                                                                   US5474921-A.
                                                                                                                                                                                                      09-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe from tyrosine-phosphorylated portion of receptor tyrosine kinase - used for detection of proteins capable of binding to receptors, useful for e.g. identifying susceptibility to cancer and diabetes
(MERI ) MERCK &
                         15-OCT-1993;
                                                 15-OCT-1993;
                                                                                                                           Rattus sp.
                                                                                                                                                    Phospholipase
                                                                                                                                                                           Phospholipase C-gamma-1.
                                                                                                                                                                                                                                                     AAR90583 standard; Protein; 1290
                                                                           12-DEC-1995
                                                                                                                                                                                                                                AAR90583;
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                                                                                                                                                                                                                                                                                                                  171 qtgmfp 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII 65
                                                                                                                                                                                                                                                                                                                                                                   q---iflrdiegvpqqptyvqalfdfdpqedgelgfrrgdfihvmdnsdpnwwkga-chg
                                                                                                                                                                                                                                                                                                                                                                                                                     lprwsrevlp--
                                                                                                                                                                                                                                                                                                                                                                                                                                            NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
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52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AA;
                                                                                                                                                                                                     (first entry)
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                                                                                                                                                 C-gamma-1; PLC-gamma-1; phosphoinositide
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                      93US-0138641
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CO INC
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RESULT 14
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Best Local S
Matches 48
                                                                                                                                                                                                  Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer; kinase substrate; immunosuppressive disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease; systemic lupus erythematosus; Vav-family.
                                                 27-MAY-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                    PKA substrate,
                                                                                                                                                                                                                                                                                                13-MAR-2000
                                                                                                                                                                                                                                                                                                                           AAY49419
                                                                                                                                                                                                                                                                                                                                                    AAY49419 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AAR90583) is obtd. by expression in a transformed bacterial host o cDNA (AAT12292) encoding rat PLC-gamma-1 and DNA coding for an epittag (Glu-Glu-Phe) which is incorporated at the C-terminus of the recombinant PLC-gamma-1 to facilitate affinity purification. The recombinant PLC-gamma-1 is used to assay the inhibitory activity of
                                                                                           27-MAY-1999;
                                                                                                                    02-DEC-1999
                                                                                                                                              WO9962315-A2
                                                                                                                                                                         Homo sapiens
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                        (LAUR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compounds towards phospho:inositide-specific phospholipase-C enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   test cpds. against PLC-gamma-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 DSEERSSWYWGRLSRQEAV-ALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYIINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPVARSRQGSGVILRQEEAEY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for expression and isolation of mammalian phospholipase a-1 - useful for determining inhibitory activity of test
                        LAURAS AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                    Vav-family protein.
                                                 98NO-0002419.
98US-0114240.
                                                                                           99WO-GB01680
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Pred. No. 6.3e-07;
32; Mismatches 85
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(JONE/)

JONES E L.

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RRESULT 1
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AC AAY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The invention provides a novel method of altering the activity of the CC protein kinase A (PKA) signaling pathway in a cell that comprises CC altering the extent of phosphorylation of one or more PKA substrates, or CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical CC compositions containing a nucleic acid molecule that encodes a PKA CC substrate, or fragment, precursor or functionally equivalent variant, CC where the sequence is modified to alter its susceptibility to PKA can be used for treating a disorder exhibiting CC phosphorylation by PKA can be used for treating a disorder sor CC infection, AIDS, common variable immunosuppressive disorders or CC infection, AIDS, common variable immunodeficiency or cancers. Conditions CC in which upregulation of the PKA pathway is required, such as autoimmune CC disease, e.g. systemic lupus erythematosus, may also be treated. The CC present sequence represents a PKA substrate, wherein the substrate is in CC protein and Vav-2 oncogene.
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Best Local
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                                                                                                                                                                                                                        LAT; tyrosine kinase; linker for activation of T cell; TCR; human; T-cell receptor; TCR signalling pathway; neoplasia; inflammation; hypersensitivity; allergy; microbial infection; genetic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 93; 111pp; English
                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of human Vav.
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                                                              WO9932627-A2
                                                                                                                                                                                            autoimmune disease; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wyagpmeragaesilanrsdgtflvrqrvkdaaefaisikynvevkhikimtaeg---- 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    845 AA;
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---lyritekkafrgltelvefygqnslkdcfksldttlqfpfkepekr 771
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27.3%;
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; Pred. No. 6.6e-07;
27; Mismatches 67;
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                                                                                                                                                                                               infection; genetic
modulator; Vav.
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                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a protein tyrosine kinase substrate LAT (linker CC for activation of T cells) protein. Modulation of interaction between LAT CC and the T-cell receptor (TCR) affects the TCR signalling pathway. LAT is CC a substrate for tyrosine kinases and becomes phosphorylated after TCR CC engagement, resulting in recruitment of other signalling molecules. LAT CC is used to identify and test (ant)agonists of tyrosine kinase signalling CC pathways, i.e. modulation of interaction between tyrosine kinase signalling CC substrates and intracellular ligands or between these ligands and other CC members of the pathway, including identification of downstream signalling CC proteins, particularly in immune system cells. These modulators are CC diseases that involve undesirable cell proliferation, differentiation, CC growth or T cell anergy, e.g. neoplasia, inflammation, hypersensitivity CC allergy, microbial infection, metabolic, genetic or autoimmune diseases, CC graft rejection. LAT is also used to generate specific antibodies, used CC for detection of LAT. Nucleic acid that encodes LAT, or its fragments, cCC are used to identify homologous sequences in other species; to detect the CLAT gene and as sources of antisense therapeutics. Modulators of LAT are cC centrially more specific and less toxic than known immunosuppressants cCC sequence of human Vav.
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                         723
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174 NAEDSEGKRGMIPVPYVEK 192
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                                                                                                                                                                                                                                     16 WYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSH--YIINSSGPRPP
                                                                                                                                                                                                                                                                                 Local Similarity nes 54; Conserv
                                                                                                                                                          VPPSPAQPPPGVSPSRLRIGDQE-FDSLPALLEFYK-----IHYLDTT---
                                                                                                                                                                                             wyagpmeragaesilanrsdgtflvrqrvkdaaefaisikynvevkhtvkimtaeg----
                                                                             -TLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQ-WW
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                                                                                                                                                                                                                                                                                                                                                                                 797 AA;
                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                10.0%; Score 172.5; DB: 27.1%; Pred. No. 8.3e-07
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                                       -akarydfcardrselslkegdiikilnkkgqqgww
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                                                                                                                                                                                                                                                                                                                  DB 20;
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